GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:23:54 ; Search time 19.4774 Seconds
                 (without alignments)
                 3287.177 Million cell updates/sec

Title: US-09-836-077-3
Perfect score: 3615
Sequence: 1 MTPPPGRAAPSAPRARVPG...........LAASLWLGVLPLTLGLLVH 666

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

arched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_73:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Match Length	DB	ID	Description
1	1353	37.4	653	2	T03102	semaphorin homolog
2	654.5	18.1	771	2	D49423	semaphorin III pre
3	632.5	17.5	772	2	A49069	collapsin - chicke
4	628.5	17.4	748	2	I48744	semaphorin A - mou
5	621	17.2	772	2	I48747	semaphorin V - hum
6	617	17.1	749	2	G01856	semaphorin A - mou
7	617	17.1	782	2	I48746	semaphorin C - mou
8	612	16.9	753	2	I58169	semaphorin III - m
9	611	16.9	753	2	G02173	semaphorin III fam
10	597.5	16.5	751	2	I48748	semaphorin E - mou
11	485.5	13.4	760	2	I48745	semaphorin B - mou
12	479.5	13.3	834	2	S66498	M-sema F protein p
13	452	12.5	730	2	JH0798	fasciclin IV precu
14	411	11.4	712	2	T27165	hypothetical prote
15	409	11.3	1074	2	JC5928	semaphorin F precu
16	408.5	11.3	711	2	A49423	semaphorin F precu
17	407	11.3	724	2	C49423	semaphorin II precu
18	399	11.0	656	2	B49423	semaphorin I - fru
19	364	10.1	441	2	S29921	hypothetical prote
20	363	10.0	403	2	E42521	A39R protein - vac
21	312	8.6	676	2	T33853	hypothetical prote
22	236.5	6.5	2051	2	T13164	plexin B - fruit f
23	228	6.3	295	2	JQ1775	Sal19R protein - v
24	215	5.9	1894	2	JC4980	plexin 1 precursor
25	190	5.3	1945	2	T13937	plexin A - fruit f
26	186	5.1	1905	2	S15553	plexin - African c
27	174	4.8	1872	2	JC4976	plexin 3 precursor
28	170	4.7	1884	2	JC4975	plexin 2 precursor
29	139	3.8	1375	1	JC5148	hepatocyte growth
30	133	3.7	1425	2	T30811	hepatocyte growth
31	129	3.6	1568	2	T09074	semaphorin recepto
32	124.5	3.4	620	2	T30765	hypothetical prote
33	122	3.4	1404	1	A48196	protein-tyrosine k
34	114	3.2	142	2	JQ1776	protein-tyrosine k
35	113.5	3.1	1376	2	G00043	SaIFIR protein - v
36	113.5	3.1	1658	2	D86890	osteonidogen - hum
37	112.5	3.1	1302	2	B41249	DNA-directed DNA p
38	111	3.1	122	2	C72169	multidrug resistan
39	111	3.1	122	2	H36852	14R protein - vari
40	109.5	3.0	1379	1	T28584	hepatocyte growth
41	109	3.0	637	2	S01254	hepatocyte growth
42	106.5	2.9	122	2	JQ2039	A46R protein - var
43	106.5	2.9	1792	2	T08878	A43R protein - var
44	105.5	2.9	622	2	S62580	superviliin P205 -
45	105.5	2.9	1271	2	T43269	probable multicopp
						microcystin synthe

ALIGNMENTS

RESULT 1
T03102
semaphorin homolog A3 - alcelaphine herpesvirus 1
C;Species: alcelaphine herpesvirus 1
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03102;
R;Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A;Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A;Reference number: Z14840; MUID:97404659; PMID:9261371
A;Accession: T03102;
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-653 <ENS>
A;Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58054.1; PID:g2337970

Query Match   37.4%; Score 1353; DB 2; Length 653;
Best Local Similarity   45.9%; Pred. No. 1.7e-95;
Matches 277; Conservative 86; Mismatches 228; Indels 12; Gaps 7;

Qy   22 PARLG-LPLRLRLLLLWAAAASAQGHLRSGGPRIFAVWKGHVGQDRVDFGQTEPHTVLFH   80
              ||| |::||:|||| : |::.||:||||| | ||| |:|||:|||.|:| ||||||||
Db   45 PAAMGTLCVSIRLLMIL-SAITAAKSRFIDKPRLIVNLTDGFGQHRF-FGPGEHHVLFH 102

Qy   81 EPGGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGSTPKGSCLDKRDCENYITLLLERSEGL 140
              ||| | ||||| ||| ||:|| ||||||||||||:.||||:.| |:.|:||:||| | |:
Db   103 SLNSSDVYVGGNNTIYLFDFAHSSNASTALINITSTHNTHRLSSTCENFITLLHNQTDGL 162

Qy   141 LACGTNARHPSCWNLVNGTVVPLGEMRGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKI 200
              ||||||:||: ||:|||||||| |:||||||::||::|:|:|||| |||:||:||||||||
Db   163 LACGTNSQKPSCWLINNLTTQFLGPKLGLAPFSPSSGNLVLFDQNDTYSTINLYKSLSGS 222

Qy   201 PRFRRIRGESELYTSDDTVWQNPQFIKATIVHQDQAYIDDKIYYFFREDNPDKNPEAPLNVS 260
              || ||: |||||||||:|||:|||||||| ||||||||||||||:|||||||:||||||
Db   223 HKFRRIAGQVELYTSDPTAMHRPQFVQATAVHKNESYDDKIYFFQENHSHSDEKQFPHTVP 282

Qy   261 RVAQLCRGDQCGGESSLSVSKWNTFLKAMLVCSDAATNKNFNRLQDVFLLDPDSGQWRDTR 320
              |||:|| || ||||||||||||:|||| ||||||:| ::|::||||:||||:|||||||
Db   283 RVGQVCSSDQGGESSLSVKWTFLKARLACVDYDTGRIYNELQDIFIWQAPENSWEETL 342

Qy   321 VYGVFSNPWNYSAVCVYSLGDIDKVFPRTSSLKGYHSSLPNPRPGKCLPDQPIPTETFQV 380
              ||||:||||||||| |::|||||||:||::|||||:|||||.||||||.||||||||:||
Db   343 IYGLFLSPWNFSAVCVFTVKDIDHVFKTSLKIKNYHHKLPTPRPGCQCMKHQHVPETFQV 402

Qy   381 ADRHPEVAQRVEPMGPLKTPLFHSKYHYQKVAVHRMQASHGETP--HVLYLTFDRGTIHK 438
              |||: ||| | :|:||| | | ::||:| : | || ||||| :: |:|| ||| |||
Db   403 ADRYPEVADPVYQKNNAMFPIIOSKYIYTKLLVYRVE--YGGVFWANIFIYLTTIKGTIHI 460

Qy   439 VVEPGEQEHSPAFNIMEIQPFRRAAAIQTMSLDAERRKLYSSQOWEVSQOVPLDLCEVYGG 498
              |:|||:|||||||| |: |: || || |||| | ||:||| |||.|:||||.||| ||
Db   461 YVRYEDSNSTTALNILEINPEQKPAPIQNILLDNTNLKLYVNSEWEVSEVPLDLCSVYGN 520

```
Qy  499 GCHGCLMSRDPYCGWDQGRCISIYSSERSVLQSINPAEP--HKECPNPKPDKAPLQKVSL 556
Db  521 DCFSCFMSRDPLCTWYNNTC---SFKQRVSVETFGGPANRTLSEMCGDHYAPTVVKHQVSI 577

Qy  557 APNSRYYLSCPEMSRHATYSWRHKENVEQSCEPGHQSPNCILFIENLTAQQYGHYFCEAQ 616
Db  578 PLLSNSYLSCPAVSNHADYFWTKDGFYEKRCHVKTHKNDCILLIANSTTATNGTHVCNMK 637

Qy  617 EGS 619
Db  638 EDS 640
```

RESULT 2
D4923
semaphorin III precursor - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: D4923
R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
Cell 75, 1389-1399, 1993
A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone
reference number; A49423; MUID:9409332; PMID:8269517
A;Reference number: A49423; MUID:9409332; PMID:8269517
A;Molecule type: mRNA
A;Residues: 1-771 <KOL>
A;Status: preliminary; nucleic acid sequence not shown
C;Genetics:
C;Cross-references: GB:L26081; NID:g799328; PIDN:AAA65938.1; PID:g436560
A;Genetics:
A;Gene: GDB:283448
A;Cross-references: GDB:SEMA1
C;Superfamily: semaphorin

Query Match   18.18;   Score 654.5;   DB 2;   Length 771;
Best Local Similarity 28.2%; Pred. No. 6.9e-42;
Matches 194; Conservative 115; Mismatches 280; Indels 99; Gaps 27;

```
Qy   32 RLLLLLWAAAASAQGHLRSG-----PRIFAVWKGHVGQDRVD-----FGQTEPHTVLFHEP 82
Db    6 RIVCLFWGVLLTARANYQNGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLDEE 65

Qy   83 GSSSVVWGGRGKVYLFDFPEGKNASVRTVNIGSTK-----GSCLDKRDCENYITLLER 135
Db   66 RSRLYVGAKDHIFSPDLVNIKDFQKIVWPVSYTRRDECKWAGKDILK-ECANFIKVLKA 123

Qy  136 RSE-GLLACGTNARHPSCWNLVNGTVVPLGEM------------RGYAPFSPDENS 178
Db  124 YNQTHLYACGTGAFHPIC------------TYIEIGIHIPEDNIFKLENSHFENGRGKSPYDKLLT 177

Qy  179 LVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT-----SDTVMQNPQFIKATIVHQ-DQ 234
Db  178 ASLLIDGELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPKFISAHLISESDN 237

Qy  235 AYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDA 294
Db  238 PEDDKVYFFFRENAIDGEHSGKATHARIGQICKNDFGGHRSL-VNKWTTFLKARLICSVP 296

Qy  295 ATN---KNFNRLQDVFLL--PDPSGQWRDTRVYGVF----SNPWNYSAVCVYSLGDIDKVF 346
Db  297 GPNGIDTHFDELQDVFLMNRKDP---KNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVF 352

Qy  347 ------RTSSLKGYHSSLPNPRPGKC-----LPDQQPIPTETFQVADRHPEVAQR 390
Db  353 LGPYAHRDGPNYQWPYQGRVPYPRPGTCPSKTFEGGFDSTKDLPDDVITFARSHPAMYNP 412

Qy  391 VEPMG----PLKTPLFHSKYHYQKVAVHRMQAASHGETFHVLYLTTDRGTIHKVVE-PGEQ 445
Db  413 VFPMNNRPIVIKTDV---NYQFTQIVVDRVDAEDGQ-YDVMFIGTDVGTVLKVVSIPKET 468

Qy  446 EHSFAFNIM-EIQOPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDICEVYGGGCHGCL 504
Db  469 WYDLEEVLLEEMTVREPTAISAMELSTKQQOLYIGSTAGVAQLPLHRCDIYGKACACECC 528
```

RESULT 3
A49069
collapsin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
C;Accession: A49069
R;Luo, Y.; Raible, D.; Raper, J.A.
Cell 75, 217-227, 1993
A;Title: Collapsin: a protein in brain that induces the collapse and paralysis of neu
A;Reference number: A49069; MUID:9406554; PMID:8402908
A;Molecule type: mRNA
A;Residues: 1-772 <LUO>
A;Status: preliminary; not compared with conceptual translation
A;Cross-references: GB:U02528; NID:g410078; PIDN:AAC59638.1; PID:g410079
C;Superfamily: semaphorin

Query Match   17.5%;   Score 632.5;   DB 2;   Length 772;
Best Local Similarity 28.4%; Pred. No. 3.3e-40;
Matches 195; Conservative 101; Mismatches 265; Indels 125; Gaps 28;

```
Qy   29 LRLRLLLLMAAAASAQGHLRSGPRIFAVWKGHVGQDR-VDF----GQTEPHTVLFHEPG 83
Db    7 IALLSIGVLLAGRVNCQHVKNNVPRLKLSYKEMLESNNIVNFNGLANSSSYHTFLDEE- 65

Qy   84 SSSVVWGGRGKVYLFDFPEGKNASVRTVNI-------GSTKGSCL-----DKRDCE 127
Db   66 RSRLYVGAKDHIFSFNL-------VNIKEYQKIVWPVSHSRDECKWAGKDILRECA 115

Qy  128 NYITLLERRSE-GLLACGTNARHPSCWNLVNGTVVPLGEM------------RGYA 170
Db  116 NFIKVLKTYNQTHLYACGTGAFHPMC------------TYIEVGSHIPEDNIFRMEDSHFENGRGKS 169

Qy  171 PFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT----SDTVMQNPQFIKA 227
Db  170 PYDPKLLITASLLVDGELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPRFISA 229

Qy  228 TIV-HQDQAYDDKIYYFFREDNDDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLK 286
Db  230 HLIPESDNPEDDKIYFFFRENAIDGEHTGKATHARIGQICKNDFGGHRSL-VNKWTTFLK 288

Qy  287 AMLVCSDAATN--KNFNRLQDVFLL--PDPSGQWRDTRVYGVF----SNPWNYSAVCVYS 338
Db  289 ARLICSVPGPGIDTHFDELQDVFLMNSKDP---KNPIVYGVFTTSSNIFKGSATGVSQLP 344

Qy  339 LGDIDKVF------RTSSLKGYHSSLPNPRPGKC-----LPDQQPIPTETFQVAD 382
Db  345 MTDVRRVFLGPYAHRDGPNYQWPYQGRVPYPRPGTCPSKTFEGGFDSTKDLPDEVITFAR 404

Qy  383 RHPEVAQRVEPMGP----LKTPLFHSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHK 438
Db  405 SHPAMYNPVFPINSRPIMIKTDV---DYQFTQIVVDRVDAEDGQ-YDVMFIGTDIGTVLK 460

Qy  439 VVE-PGEQEHSFAFNIM-EIQOPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDICEVY 496
Db  461 VVSIPKETWHELEEVLLEEMTVREPTVISAMKISTKQQOLYIGSATGVSQLPLHRCDVY 520

Qy  497 GGGCHGCLMSRDPYCGWDQGRCISIY--SSERSVLQSINPAEPHKEC------PNPKPDK 548
Db  521 GKACAECCLARDPYCAWDGSSCSRYFPTAKRRTRRQDIRNGDPLTHCSDLQHHDNPSGQT 580

Qy  505 MSRDPYCGWDQGRCISIY--SSERSVLQSINPAEPHKECPNPKPDK-----APLQKVSL-A 557
Db  529 LARDPYCAWDGSACSRYFPTAKRRTRRQDIRNGDPLTHCSDLHHDNHGHSPEERIIGV 588

Qy  558 PNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCI-----LFIENLTAQQYGHYF 612
Db  589 ENSSTFLECSPKSQRALVYWQFQRNEERKEEIRVDDHIIRTDQGLLLRSLQOKIDSGNYL 648

Qy  613 CEAQEGSYFREAQHWQLLPEDGIMAEHL 640
Db  649 CHAVEHGFIQTLLKYTL--EVIDFEHL 673
```

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Qy   549 APLQKVSLAPNSRYYLSCPMESRHATYSWR--------HKENVEQS-----CEPGHQSPNC 596
         : | :|:  |       |:||   | | |           :|   |:|      | :| |
Db   581 LEEKIIYGVENSSTFLECSPKSQRAIVYWQFQKQNDDHKVEIKVDDRMIRTEQG------ 634

Qy   597 ILFIENLTAQQYGHYFCEAQEGSYFR 622
         | |:|| |  | || || | :|:
Db   635 -LLLRSLQRRDSGIYFCHAVEHGFIQ 659
```

RESULT 4

I48744

semaphorin A - mouse

C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I48744
A;Reference number: I48744; MUID:95267431; PMID:7748561
R;Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates
A;Accession: I48744
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-748 <RES>
A;Cross-references: EMBL:X85990; MUID:95267431; PMID:7748561; PIDN:CAA59982.1; PID:g854324
C;Genetics:
A;Gene: semA
C;Superfamily: semaphorin

```
Query Match             17.4%;   Score 628.5;   DB 2;   Length 748;
Best Local Similarity   31.5%;     Pred. No. 6.5e-40;
Matches  181;   Conservative  76;   Mismatches  244;   Indels  73;   Gaps  21;

Qy   125 DCENYITLLERSE-GLLACGTNARHPSC-------WNLVNGTVVPLG------EMRGYAPFSP 174
         : | ||   |:  ||  | |  |  |         |: | |: :|       ::  |  |
Db   112 ECMNFVRLLHAYNHTHLLACRTGAFHPTCALWRWATAGGTHASTGPEKLEDGKGKTPYDP 171

Qy   175 DENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT----SDTVWQNPQFIKA-TIV 230
         |   :|| |:|    |     | | | |  | :|  |       ||| |:|  |:|  :|
Db   172 RHRPPSVLVGEELYSGVTADLMGRDFTIFRSLGQNPSLRTEPHDSRWLNEPKPVKVFWIP 231

Qy   231 HQDQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQLCRGDQQGGESSLSVSKWNTFLKAML 289
         | |  |  |||:|   ||  |:|       |||| |||| |||| |||| :|  ||||
Db   232 ESENPDDDKIYFFFRESAVEEAPAFAMGRMSVSRVGQICRNDLGGQRSL-VNKWTTFLKARL 290

Qy   290 VCS--DAATNKNFNRLQDVFLLPDPSGQWRDT-RVYGVFSNP---WNYSAVCVYSLGDID 343
         |      |:| | ||| || :|     :||       | |:|     |:| | |: ||:|
Db   291 VCSVPGVBEGDTHFDLQDVFLL---SSRDQTPLLYAVFSTSSGVFQGSAVCVYSMNDVR 347

Qy   344 KVF---------RTSSLKGYHSSLPNRPRGKC------LPDQQPIPTETFQVADRHPEV 387
         ||           |||| |||||| || | |      | :|  | | | | |  | |
Db   348 RAFLGPLPHKEGPTHQWVSYQGRVPYPRPGMCPSKTFGTFSSTKDFPDDVIQFGRNHPLM 407

Qy   388 AQRVEPMCGPLKTPLF----HSKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKV--VEP 442
         |  : | |  | | |      ::|:| ||| || || ||| ||:|||||||||:|   |:|
Db   408 YNPVLPMG--GRPLFLQVGAGYFTQIAADRVAAADGH-YDVLFIGTDVGTVLKVISVPK 464

Qy   443 GEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHG 502
         |:|| || |:|  ||| ||||| | || |:|||||||| ||||| ||| ||| |  | |
Db   465 GRRPNSEGLLEELQVFEDSAAITSMQISSKRQQLYVASRAVAQIALHRCTALGRACAE 524

Qy   503 CLMSRDPYCGWDQGRCISIY--SSERSVLQSINPAEPHKECPNPKPDKAPLQKVSLAPNS 560
         ||:|| | ||| || || |    || ||||| ||| |||| | ||  ||| | |   ||
Db   525 CCLARDPYCAWDGSACTRFQPTPAKRRRRRQDIRNGDPSTLCSGSDSSHSVLLEKKVLGVES 584

Qy   561 -RYYLSCPMESRHATYSWRH---------KENVEQSCEPGHQSPNCILFIENLTAQ 606
         ||| ||| ||||||| | | :       ::| |:|   | : ||| | |:||  |
Db   585 GSAFLECSPERSLQAHVQWTFEQGAGEAAHTQVLAEERVERTARG----LLIRGLRRQ 636

Qy   607 QYGHYFCEAQEGSYFRFAQHWQLLPEDGIMAEHL 640
         | |||||| |:|:||  ||| |||| | |||| |
Db   637 DSGVYLCVAVEQGFSQPLRRLVLHVLSAAQAERL 670
```

RESULT 5

I48747

semaphorin D - mouse

C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I48747
A;Reference number: I48747; MUID:95267431; PMID:7748561
R;Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat...
A;Accession: I48747
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-772 <RES>
A;Cross-references: EMBL:X85993; MUID:95267431; PMID:7748561; NID:g854329; PIDN:CAA59985.1; PID:g854330
C;Genetics:
A;Gene: semD
C;Superfamily: semaphorin

```
Query Match             17.2%;   Score 621;   DB 2;   Length 772;
Best Local Similarity   27.5%;     Pred. No. 2.5e-39;
Matches  189;   Conservative  110;   Mismatches  283;   Indels  106;   Gaps  27;

Qy    36 LLWAAAASAQGHLRSG----PRIFAVWKGHVGQDRVD-------FGQTEPHVLFHBPGSSS 86
         | |   :: || | |      ||:|  |:|  || :|       || |:||:||  |:||
Db    10 LFWGVLLTARANYANGKNNVPRLKLSYKEMLESNNVITENGLANSSSYHFFLLDEE-RSR 68

Qy    87 VWVGGRGKVYLFDFPEGKNASVRTVNIGSTK----------GSCLDKRDCENYITLLERSE- 138
         ||: |  : :|   | :|    :: :|  :|           || | :::| |  :|| ::
Db    69 LYVGAKDHIFESFNLVNIKDFQKIVWPVSYTRRDECKWAGKDILK-ECANFIKVLEAYNQT 127

Qy   139 GLLACGTNARHPSCWNLVNGTVVPLGEM-------------------RGYAPFSPDENSLVLF 182
         :|:ACGT A HP C   ::: | :  |                    ||: |     :|::|
Db   128 HLYACGTGAFHPIC-----TYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLL 181

Qy   183 EGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVWQNPQFIKATIV-HQDQAYDD 238
          :|| || |  : |  ||| || || :| || | ||| |:|  |::|  : | |  :|
Db   182 IDGELYSGTAADFMGRDFAIFRTLGDHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDD 241

Qy   239 KIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQQGGESSLSVSKWNTFLKAMLVCSDAATN- 297
         | |:||||:    | | :  || | ::| :|  ||  :||::| :|| |||  | | |:
Db   242 KVYFFFRENAIGGEHSGKATHARIGQICKNDFGGHRSL-VNKWTTFLKARLICSVPGPGNG 300

Qy   298 --KNENRLQDVFLL--PDPSGQWRDTRVYGVF----SNPWNYSAVCVYSLGDIDKVE---- 346
           :  ::|QDVFL    ||     : | ||     ||  : ||||:||: |:  :|
Db   301 IDTHFDELQDVFLMNSKDP-----KNPIVGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPY 356

Qy   347 -----RTSSLKGYHSSLPNRPRGKC--------LPDQQPIPTETFQVADRHPEVAQRVEPM 394
              | |  |  |||| || |  |        |||::| | | | | |  | |  :| |:
Db   357 AHRDGPNYQWWPYQGRVPYPRPGTGCPSKTFGGFDSTKDLPDDVITFGCRSHPAMYNPVFPI 416

Qy   395 G-----PLKTPLFHSRKYHYQKVAVHRMQASHGETFHVLYLTTDRGTIHKVVE-PGEQEHSF 449
               ||:| ||   ::|:| ||| || || ||| ||:|||||||||:| | | |::|
Db   417 NNRPIMIKTDV----NYQFTQIVDRVDAEDGQ-YDVMFIGTDVGTVLKVVSVPKETWHDL 472

Qy   450 AFNIM-EIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCHGCLMSRD 508
          :::: |:  |  |: | | :|  :|:|||:|| | |:| ||| |::|| || || ||
Db   473 EEVLLEEMTVFREPTTISAMELSTKQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARD 532

Qy   509 PYCGWDQGRCISIY--SSERSVLQSINPAEPHKECPN-------PKPDKAPLQKVSLA 557
         |||:WD   | | :    | || ||||| ||| ||         ||   | | :  :
Db   533 PYCAWDGSSCSRYFPTAKRRTRRQDIRNGDPLTHCSDLEDHDNHHGPSLEBERIIGVSE- 590

Qy   558 PNSRYYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCI-----LFIENLTAQQYGHYF 612
           | ::| || || || | | :  :: |||| | : :|      | |:|  | | :|:|
Db   591 -NSSTFLECSPKSQRALVWQFQRRNRRSKREIRMGDHIIRTEQGLLLRSLQKIDSGNYL 649

Qy   613 CEAQEGSYFRFEAQHWQLLPEDGIMAEHL 640
         | | |||:|   | | :||| |:| |||
Db   650 CHAVEHGFMQTLLKYTL---EVIDTEHL 674
```

RESULT 6
G01856
semaphorin V - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
R;Sekido, Y.
R:Sekido, Y.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08634
A;Accession: G01856
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: G01856
A;Molecule type: mRNA
A;Cross-references: EMBL:U28369; NID:g974283; PIDN:AAD09138.1; PID:g974284
A;Residues: 1-749 <SEK>
A:Genetics:
C;Superfamily: semaphorin

Query Match   17.1%;   Score 617; DB 2; Length 749;
Best Local Similarity 28.2%;   Pred. No. 4.9e-39;
Matches 202; Conservative 92; Mismatches 293; Indels 130; Gaps 27;

```
Qy    7 GRAAPSAPRARVPGPPARLGLPLRLRLLLLWA----AAASAQGHLRSGPRIFAVWKGHV 62
          ||| ||  : ||  |   |   |       |
Db    2 GRAGAAAV---IPG-----------LALLWAVGLGSAAPSPPRLRLSFQELQAWH--- 42

Qy   63 GQDRVDFGGQTFPHTVLFHEPEGSSSVVWGRGKVYLFDFPEGKNASVRTVNI------- 113
Db   43 GLQTFSLERTCCYQALLVDEERGRLFVGAENHVASLNL---DNISKRAKKLAWPAPVEWR 99

Qy  114 -----GSTKGSSCLDKRDCENYITLLERRSE-GLLACGTNARHPSCWNLVNGTVVPLG-- 164
Db  100 EECNWAGKDIGT-----ECMNEVKLLHAYNRTHLLACGTGAFHPTC----AFVEVGHR 148

Qy  165 --------EMRGYAFFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGES 210
Db  149 AEEPVLRLDPGRIEDGCGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGORP 208

Qy  211 ELYT---SDTVMQNPQFIKA-TIVHQQAYDDKIYYFFREDNPDKNPE-APLNVSRVAQL 265
Db  209 SLRTEPHDSRWLNEPKFVKVFWIPESENPDDKIYFFFRETAVEAAPALGRLSVSRVGQI 268

Qy  266 CRGDQDGGGESSLSVSKWNTFLKAMLVCS--DAATNKNFNRLQDVFLLPDPSGQWRDTRVYG 323
Db  269 CRNDVGGQRSL-VNKWTTFLKARLVCSVPGVEGDTHFDQLQDVFLL--SSRDHRTPLLYA 325

Qy  324 VFSNP---WNYSAVCVYSLGDIDKVF----------RTSSLKGYHSSLPNPRPGKC---- 366
Db  326 VFSTSSIFQGSAVCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPVPRPGMCPSKTF 385

Qy  367 --LPDQOPIPTETFQVADRHPEVAQRVEPMGPLKTPLF---HSKYHYQKAVAHRMQASHG 421
Db  386 GTFSSTKDFPDDVIQFARNHPLMYNSVLPTG---GRPLFLQVGANYTFTQIRAADRVAAADG 443

Qy  422 ETFHVLYLTTDRGTIHKV----VEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYV 479
Db  444 H-YDVLFIGTDVGTVLKVISVPKGSRPSAEGLLLEELHVFEDSAAVTSMOISSKROLYV 502

Qy  480 SSQWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQGRCISIYSS--ERSVLQSINPAEP 537
Db  503 ASRSAVAQIALHRCAAAHGRVCTECCLARDPYCAWDGVACTRFQPSAKRRFRRQDVRNGDP 562

Qy  538 HKECPNPKDKAPLQ-KVSLAPNSRYLSCPMESRHATYSWRH--------------KENV 583
Db  563 STLCSGDSSRPALLEHKVFGVEGSSAAFLECEPRSLQARVEWTFQRAGVTAHTQVLAEERT 622

Qy  584 EQSCEPGHQSPNCLLFIENLTAQYGHYFCEAQGGSYFREAQHWQLLPEDGIMAEHL 640
Db  623 ERTARG-------LLLRLRRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAERL 671
```

RESULT 7
I48745
semaphorin C - mouse (fragment)
C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000
C;Accession: I48746
R;Püschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat
A;Reference number: I48746; MUID:95267431; PMID:7748561
A;Accession: I48746
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-782 <RES>
A;Cross-references: EMBL:X85992; NID:g8543327; PIDN:CAA59984.1; PID:g8543328
A;Genetics:
A;Gene: semC
C;Superfamily: semaphorin

Query Match   17.1%;   Score 617; DB 2; Length 782;
Best Local Similarity 30.4%;   Pred. No. 5.2e-39;
Matches 193; Conservative 91; Mismatches 253; Indels 98; Gaps 28;

```
Qy   75 HTVLFHEPGGSSSVVWGRGKVYLFD-------FPEGKNASVRTVNIGSTKGSCL-----DKR 124
Db   16 YTALLLSQDGKTLVVGARELALFALNSNLSFLPGGEYQELLWSADADRKQQCSFKGKDPKR 75

Qy  125 DCENYI-TLLERRSEGLLACGTNARHPSC-------WNLVN--GTVVPLGEMRGYAFFS 173
Db   76 DCQNYIKILLPLNSSHLLTCGTAAFSPLCAYIHIASFTLAQDEAGNVI-LEDGKGHCPFD 134

Qy  174 PDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTV--MQNPQFIKATIVH 231
Db  135 PNFKSTALVVDGELY-TGTVSSFQGNDPAISRSQSSRPTKESSLNWLQDPAFVASATSP 193

Qy  232 QDQAY----DDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQDGGGESSLSVSKWNTFLKA 287
Db  194 ESLGSPIGDDDKIYFFFSETGQEFEFFENTIVSRVARVCKGDEGGERVLQ-QRWTSFLKA 252

Qy  288 MLVCSDAATNKNFNRLQDVFLL-PDPSGQWRDTRVYGVFSNPWNY-----SAVCVYSLGD 341
Db  253 QLLCSRPDDGFPENVLQDVFTLNPNPQ-DWRKTLSIGVFTSQWHRGTTEGSAICVFTMND 311

Qy  342 IDKVF-------RTSSLKGYHSSLPNPRPGKCLPD--QQPIPTETFQVADR------- 383
Db  312 VQKAFDGLYKVKVNRETQQWYTEHQVPPRPGACITNSARERKINSSLQLPDRVLNFLKD 371

Qy  384 ----HPEVAQRVEPMGPLKTPLFHSKYHYQKAVAHRMQASHGETFHVLYLTTDRGTIHKV 439
Db  372 HFLMDGQVRSRLLLLQP-------RARYQRVAVHRVPGLH-STYDVLFGTGDGRLHKA 422

Qy  440 VEPGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGG 499
Db  423 VTLSSRVHI----IEELQIFPQGQPVQNLLDSHGGLLYASSHSGVQVPVANCSLY-PT 477

Qy  500 CHGCLMSRDPYCGWDQGRC--ISIYS---SERSVLQSINPAEPHKECPNPK------PD 547
Db  478 CGDCLLARDPYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARFLVPG 537

Qy  548 KAPLQKVSLAPNSRYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNC-ILFIENL--- 603
Db  538 K-PCKQVQIOPNTVNTLACPLLSNLATRLWVH------NGAPVNASASCRVLPTGDLLIV 590

Qy  604 -TAQQYGHYFC-EAQEGSYFREAQHWQLLPEDGIM 636
Db  591 GSQQGLGVFQCWSIEEGFQQLVASYCPEVMEEGVM 625
```

RESULT 8
I58169
semaphorin III - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
R;Messersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.;
Neuron 14, 949-959, 1995
A;Title: Semaphorin III can function as a selective chemorepellent to pattern sensory

```
A;Reference number: 158169; MUID:95267432; PMID:7748562
A;Accession: 158169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-666 <RES>
A;Cross-references: GB:L40484; NID:g703189; PIDN:AAA73934.1; PID:g703190
C;Genetics:
C;Gene: SemaIII
C;Superfamily: semaphorin

Query Match           16.9%;  Score 612;  DB 2;  Length 666;
Best Local Similarity 29.4%;  Pred. No. 1e-38;
Matches 173;  Conservative 91;  Mismatches 227;  Indels 98;  Gaps 23;

Qy  124  RDCENYITLLERRSE-GLLACGTNARHPSCWNLVNGTVVVPLGEM--------------  166
Db    6  KECANFIKVLEAYNQTHLYACGTGAFHPIC------------------YIEVGHHPEDNIFKLQDSHFENG  59

Qy  167  RGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIGESELYT---SDTVMQNPQ  223
Db   60  RGKSPYDPKLLTASLLIDGELYSGTAANFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPR  119

Qy  224  FIKATIV-HQDQAYDDKIYYFFREDNDENPEAPLNVSRVAQLCRGDGQGGESSLSVSKWN  282
Db  120  FISAHLIPESDNPEDDKVYFFRENAIDGEHSGKATHARIGQICKNDPGGHRSL-VNKWT  178

Qy  283  TFLKAMLVCSDAATN------KNFNRLQDVFLL--PDPSGQWRDTRVYGVF------SNPWNYSAV  334
Db  179  TFLKARLICSVPGPNGIDTHFEDLQDVFLMNSKDP---KNPIVYGVFTTSSNIFKGSAV  234

Qy  335  CVYSLGDIDKVFRTSSLKG----------YHSSLPNPRPGKC-----LPDQQPI  373
Db  235  CMYSMSDVRRV-----------LLGPYAHRDGPNYQWPVPQGRVYPVPRPGTCPFSKTFGGFDSTKDL  289

Qy  374  PTETFQVADRHPEVAQRVEPMG---PLKTPLFHSKYHYQKVAVHRMQASHGETFHVLYL  429
Db  290  PDDVIFPARSHPAMYNVFPINNRPIMIKTDV---NYQFTQIVVDRVDAEDGQ-YDVMFI  345

Qy  430  TTDRGTIHKVVE-PGEQEHSFAFNIM-EIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQ  487
Db  346  GTDVGTVLKVVSVPKETWHDLEEVLLEEMTVREPTTISAMELSTKQQLYIGSTAGVAQ  405

Qy  488  VPLDLCEVYGGGCGHGCLMSRDPYCGWDOGRCISIY---SSERSVLQSINPAEPHKECPN--  543
Db  406  LPLHRCDIYGKACAECCLARDPYCAWDGSSCSRYFPTAKRRTRRQDIRNGDPLTHCSDLQ  465

Qy  544  -------PKPDKAPLQKVSLAPNSRYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNC  596
Db  466  NSSTFLECSPKSQRALVYWQFQRRNEDRKEEIKMGDHI  522

Qy  466  HHDNHHGSLEERIIYGVE---NSSTFLECSPKSQRALVYWQFQRRNEDRKEEIKMGDHI  522
Db  466  PKPDKAPLQKVSLAPNSRYLSCPMESRHATYSWRHKENVEQSCEPGHQSPNC  596

Qy  597  I-----LFIENLTAQQYGHYFCEAQEGSYFREAQHWQLLPEDGIMAEHL  640
Db  523  IRTEQGLLRSLQKKDGSNYLCHAVEHGFMQTLLKVTL--EVIDTEHL  568
```

```
RESULT 9
G02173
semaphorin III family homolog - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C;Accession: G02173
R;Naylor, S.
submitted to the EMBL Data Library, October 1995
A;Reference number: G09275
A;Accession: G02173
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-753 <NAY>
A;Cross-references: EMBL:U38276; NID:g1061350; PIDN:AAB18276.1; PID:g1061351

Query Match           16.9%;  Score 611;  DB 2;  Length 753;
Best Local Similarity 26.9%;  Pred. No. 1.4e-38;
```

```
Matches 192;  Conservative 116;  Mismatches 281;  Indels 124;  Gaps 30;

Qy  124  RDCENYITLLERRSE-GLLACGTNARHPSCWNLVNGT------VVP--LGEMRGYAPFSPDENSLVLFE  183
Db  125  WNRTH-LYVCGTGAYNPMCTYVNRGRRAQDYIFYLEPERLESGKGGKCPYDPKLDTASALI  183

Qy  184  GDEVYSTIRKQEYNGKIPRFRRIGESELYT---SDTVMQNPQFIKATIVHQPQQAYDDKI  240
Db  184  NEELYAGVIDFMGTDAAIFRTLGKQTAMRTDQYNSRWLNDPSFIHAELIPDSAENDDKL  243

Qy  241  YYFFREDNDKNPEAPLNVSRVAQLCRGDGQGGESSLSVSKWNTFLKAMLVCS---DAATN  297
Db  244  YFFFRERSAEA-PQSPAVYARIGRICLNDDGGHCCL-VNKWSTFIKARLVCSVPGEDGIE  301

Qy  298  KNFNRLQDVFLLPDDSGQWRDTR---VYGVFSNP---WNYSAVCYSLGDIDKVFR----  347
Db  302  THFDELQDVEV-----QQTQDVRNPVIYAVFTSGGSVFRGSAVCVYSMADIRMVENGPFA  356

Qy  348  -----TSSLKGYHSSLPNPRPGKC-----LPDQQPIPTETFQVADRHPEVAQRVEPM  394
Db  357  HKEGPNYQWMPFSGKMPYPRPGTCPGGTGTFPSMKSTKDYPDEVINFMRSHPLMQVAVYPL  416

Qy  395  GPLKTPLF----HSKYHYQKVAVHRMQASHGETFHVLYLYLTTDRGTIHKV-VEPGEQEHSFA  450
Db  417  --QRRPLVVRTGAPYVRLTTIAVDQVDSADGR-YEVLFLGTDRGTVQKVIVLPKDDQEMEE  473

Qy  451  FNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCGHGCLMSRDPY  510
Db  474  LMLEEVEVKRDPAPVKTMTISSKRQQLYASASAVGVTHLSLHRCQAYGAACADCCLARDPY  533

Qy  511  CGWDOGRCISIY---SSERSVLQSINPAEPHKECP--NPKPDKAPLQKVSL-APNSRYL  564
Db  534  CAWD-GQACSRYTASSKRSRRQDVRHGNPIRQCRGFNSNANKNAVESVQYGVAGSAAFL  592

Qy  565  SCPMESRHATYSW-------RHKE-------NVEQSCEPGHQSPNCLFIENLTAQQY  608
Db  593  ECQPRSPQATVKWLFQRDPGCDRREIRAEDRFLRTEQG-------LLLRALQLSDR  641

Qy  609  GHYFCEAQEGSYFREAQHWQLLPEDGIMAEHLLGHACALAAASLWLGVLPFLTL  661
Db  642  GLYSCTATENNFKHVVTRVQL-----------HVLGRDAVHAA------LFPPLSM  680
```

```
RESULT 10
I48748
semaphorin E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I48748
R;Puschel, A.W.; Adams, R.H.; Betz, H.
R;Neuron 14, 941-948, 1995
A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat
A;Reference number: I48748; MUID:95267431; PMID:7748561
A;Accession: I48748
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-751 <RES>
A;Cross-references: EMBL:X85994; NID:g854331; PIDN:CAA59986.1; PID:g854332
C;Genetics:
A;Gene: semE
C;Superfamily: semaphorin

Query Match           16.5%;  Score 597.5;  DB 2;  Length 751;
Best Local Similarity 28.8%;  Pred. No. 1.5e-37;
Matches 175;  Conservative 96;  Mismatches 265;  Indels 71;  Gaps 23;
```

```
RESULT 11
I48745
semaphorin B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
chel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates
A;Reference number: I48744; MUID:9526749431; PMID:7748561
A;Accession: I48745
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-760 <RES>
A;Cross-references: EMBL:X85991; NID:g854325; PIDN:CAA59983.1; PID:g854326
A;Genetics:
A;Gene: semB
C;Superfamily: semaphorin

Query Match             13.4%;  Score 485.5;  DB 2;  Length 760;
Best Local Similarity   27.0%;  Pred. No. 5.9e-29;
Matches  198;  Conservative 105;  Mismatches 287;  Indels 143;  Gaps 38;

Qy   75 HTVLFHEPGSSSVVWGGRGKVYLFDPEPEGKNAS--------VRTVNIGSTKGSCLD-KR 124
         :||| || |       ::| :::|             ||| ::||| ::
Db   54 YRILLMDEDQDRIYVGSKDHILSLNI---NNISQEPLSVFWPASTIKVEECKMAGKDPTH 110

Qy  125 DCENYITLLER-RSEGLLACGTNARHPSCWNLVNG-----TVVPLGEM----RGYAPFSP 174
         ||||| || || ||| ||| :|
Db  111 GCGNEVRVVIQTFNRTHLYVCCGSGAFSPVCTYLNRGRRSEDQVFMIDSKCESSGKGRCSFNP 170

Qy  175 DENSLVLFEGDEVYSTIRKQEYNGKIPRFRRIRGESELYT---SDTVMQNPQFIKATIVH 231
         ::|: |:|||| |||:::::|:|| || | || | :|||    | |||:|| |||||
Db  171 NVNTVSVMINEELFGSMYIDFMGTDAAIFRSLTKRMQLRTDQHNSKWLSEPMFVDAHVIP 230

Qy  232 Q-DQAYDDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDGQGGGESSLSVSKWNTFLKAMLV 290
         : | :|||||| ||| ||||||||||||||||| ||||||| ||||| ||||||||||||
Db  231 DGTDPNDAKVYFFKERLTDNNRSTKQIHSMIARICPNDTGQQRSL-VNKWTTFLKARLV 289

Qy  291 CS---DAATNKNFNRLQDVFLLPDPSGQWRDTRVGVF---SNPWNYSAVCVYSIGDIDK 344
         ||   : : |||| |||||||||| |:|| || |:|    |  || ||||||:| |: |
Db  290 CSVTDEDGPETHFDELEDVFLLETDNP--RTTLVYGIFTTSSSVFKGSAVCVYHLSDIQT 347

Qy  345 VFR------------TSSLKGYHSSLPNPRPGKC----LPDQQPIPTETFQVADRHPEV 387
         |||             ||| | |||  |||| |     ||| ||| | ||: | :|| |
Db  348 VFNGPFAHKEGPNHQLISYQGRIPYPRPGTCPGGAFTPNMRTTKDFPDDVVTFIRNHPLM 407

Qy  388 AQRVEPMGPLKTPL--FHSKYHYQKVAVAHRMQAASHGETFHVLYLTTDRGTIHKVVE-PG 443
         :   ||| |   |   :||  :|:|:||    |  |||| |||| | ||||| :||||  |
Db  408 YNSISPIH--RRPLIVRIGTDYKYRIAVDRVNAADGR-YHVLFLGTDRGTVQKVVVVLPT 464

Qy  444 EQEHSFAFNIMEIQFPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGCHGC 503
         ||| ||||||||| |||||||||||||||||||||||||:|||||||||||||| || |
Db  465 NSSAGELILEBELEVFKNHVPITTMEISSKKQQLYVSSNEGVSQVSLHRCHIYGTACADC 524

Qy  504 LMSRDPYCGWDQGRCISIY---SSERSVLQSINPAEPHKECP--NPKPDKAPLQKVSL-AP 558
         :  ||||| ||  ||||:|    |:| |||||||||||||||   ||| |||||||:| ||
Db  525 CLARDPYCAWDGHSCSRFYPTGKRRSRRQDVRHGNPLTQCRGFNLKAYRNAAEIVQYGVR 584

Qy  559 NSRYVLSCPMESRHATYSWRHKENVEQSCEPGHQSPNCI----LFIENLTAQQYGHYFC 613
         | | :| | | ||| ||| :|::: : |||| || ||       ::| : |:| |: |
Db  585 NNSTFLECAPKSPQASIKWLLQKDKDRRKE-GKLNERIATSQGLLIRSVQDSDQGLYHC 643

Qy  614 EAQEGSY 620
         ||:| |
Db  644 IATENSF 650
```

```
RESULT 12
S66498
M-sema F protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999
R;Inagaki, S.; Furuyama, T.; Iwahashi, Y.
FEBS Lett. 370, 269-272, 1995
A;Title: Identification of a member of mouse semaphorin family.
A;Reference number: S66498; MUID:95385809; PMID:7656991
A;Accession: S66498
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-834 <INA>
A;Cross-references: EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110599
A;Superfamily: semaphorin
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-834/Product: M-sema F protein #status predicted <MAT>

Query Match             13.3%;  Score 479.5;  DB 2;  Length 834;
Best Local Similarity   25.6%;  Pred. No. 2e-28;
Matches  182;  Conservative 108;  Mismatches 307;  Indels 113;  Gaps 30;

Qy   86 SVWVGGRGKVYLFD------FPEGKN----ASVRTVNIGSTKGSCLDKR------DCENYI 130
         :: |||||| || |      |||||     ||:||||||||||||||:|       |||||
Db   75 TLIVGARETVLALNIQNPGIPRLKNMIPWPASER-------KKTECAFRKKSNETQCFNFI 128

Qy  131 -TLLERRSEGLLACGTNARHPSCW--NLVNGTVVPL----GEMRGYAPFSPDENSLVLF 182
          : | || ||| ||| ||:|||     : | :: |     ||  | |    :: |: |
Db  129 RVLVSYNATHLYACGTPAFSPACTFIELQDSLLLPILIDKVMDGKGQSPLTLFTSTQAVL 188

Qy  183 EGDEVYSTIRKQEYNGKIPRFRRIRGESELYTSDTVMQNPQFIKATIVHQDQAY----- 236
         || :|||   : | | :|| | | || |   |    : :|| |:| :
Db  189 VDGMLYSG-TMNNFLGSEPILMRTLG------SHPVLKTDIFLR--WLHADASFVAAIPS 239

Qy  237 DDKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDGQGGGESSLSVSKWNTFLKAMLVCSDAAT 296
         ::|:|||| |   :| || || ||||| |  | | | ||: ||| ||||||||:| |:   :
Db  240 TQVVYFFFEETASEFDFEEELYISRVAQVCKNDVGGEKLLQ-KKWTTFLKAQLLCAQPG- 297

Qy  297 NKNFNRLQDVFLLPDPSGQWRDTRVGVPSNPWNY-----SAVCVYSIGDIDKVFR---- 347
           : ||  ||:||| |:  |  ||   : :| |       |||| ||: |:|:|:
Db  298 QLPFNIIRHAVLLPADSPS--VSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVFKGNYK 355

Qy  348 ------TSSLKGYHSSLNPRPGKCLPDQQPIPTETFQ--VADRHPEVAQRVEPMGPLK 398
               | ||: | |||  |||| |  |    |||| |    |   |  ::|: ||: |
Db  356 ELNKETSRWTTYRGSEVSPRPGCSCSMGPSSDKALTFMKDHFLMDEH-------VVG 404

Qy  399 TPLF-HSKYHYQKVAVAHRMQAASHGETFHVLYLTTDRGTIHKVVEPGEQEHSFAFNIMEIQ 457
         ||   : : :| ||||   | |   ||| |: || ||||:|| |: || ||  :  : | |:
Db  405 TPLLVKSGVEYTRLAVESARGLDGSSHVVMYLGTSTGPLHKAVVP--QDSSAYLVEBIQ 461

Qy  458 PFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGCHGCLMSRDPYCGWD-QG 516
          |::||  |::  |   | | | |  : :  |:  |||| ||  | : |||| ||   |
Db  462 LSPDSEPVRNLQLAPAQGAVFAGFSGGIWRVPRANCSVY-ESCVDCVLARDPHCAWDPES 520

Qy  517 RCISIYS-SERSVLQSINPAEPHKECP------NPKPDKAP--LQKVSLAPNSRYYLSCP 567
         | | | | |:| ||| ||||||||||       ||| |||   : :    |||| ||||
Db  521 RLCGSLLSGSTKPWRQDMERGNPEWVCTRGPMARSPRQSPPQLIKEVLTVPNSILELRCP 580

Qy  568 MESRHATYSWRH-KENVEQSCEPGHQSPNCILFIENLTAQQYGHYFCEAQEGSY-FREAQ 625
          :|  |:| | |  : :   | |: :  | ::    |  | | |  | | ||   |:
Db  581 HLSALASYHWSHGRAKISEASATVYNGSLLLLPQDGVG---GLYQCVATENGYSYPVVS 636

Qy  626 HW------QLLPE-DGIMAEHL-----LGHACALAA--SLW------------LG 654
         ||      |  |   |  |       |  | |       ||            ||
Db  637 YWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSVWPHFLIVTVLLAIVLLG 696

Qy  655 VLPTL---TLGLL 664
         |: |    || ||
Db  697 VITLLLASPLGAL 709
```

```
Query Match             13.8%;  Score 479.5;  DB 2;  Length 834;
Best Local Similarity   25.6%;  Pred. No. 2e-28;
Matches  182;  Conservative 108;  Mismatches 307;  Indels 113;  Gaps 30;

Qy   37 LWAAAASAQGHLRSGPRIFAVWKGHVGQDRVDFGQTEPHTVLFHEPG--------S 84
```

```
Query Match             13.8%;  Score 485.5;  DB 2;  Length 760;
Best Local Similarity   27.0%;  Pred. No. 5.9e-29;
Matches  198;  Conservative 105;  Mismatches 287;  Indels 143;  Gaps 38;

Qy   32 RLILLIWAAAASAQGHLRSGPRIFAVWKGHVGQDR--VDF----GQTEPHTVLFHEPGSS 85
         :||   |    |     | ||   :    :||:|:             | ||| |:|||
Db   20 QLFLLPSLPPASGTGQGPMPRV----KYHAGDGHRALSFFQQKGKLRDFDTLLLSDDG-N 74
```

RESULT 13
JH0798

fasciclin IV precursor - American bird grasshopper
C;Species: Schistocerca americana (American bird grasshopper)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: JH0798
R;Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good
Neuron 9, 831-845, 1992
A;Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in
A;Reference number: JH0798; MUID:93040225; PMID:1418998
A;Accession: JH0798
A;Molecule type: mRNA
A;Residues: 1-730 <KOL>
A;Cross-references: GB:L00709; NID:g160844; PID:g160845
A;Experimental source: embryo
C;Keywords: glycoprotein; signal sequence; transmembrane protein
C;Comment: This protein plays a role in growth cone guidance in the developing central n
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-730/Product: fasciclin IV #status predicted <MAT>
F;23-627/Domain: extracellular #status predicted <EXT>
F;628-652/Domain: transmembrane #status predicted <TMM>
F;653-730/Domain: intracellular #status predicted <INT>
F;44,71,163,267,360,559/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   12.5%; Score 452; DB 2; Length 730;
Best Local Similarity   157; Conservative   89; Mismatches 229; Indels   94; Gaps   28;

Db   7 VWLLAAGLWG-LGIGAE------MWWNLVPRKTVSSGELVYVVRRFSQTGIQDFLTLTLEHS 62
                :|| || :::|| || : | :|| : | | : : | :|
Qy   85 SSVVVGGRGKVYLFDFPEGKNASVRTVNI------------------GSTKGSCLDK-----RDCENYI 130

Db   63 GLLIYVGAREALFAF------------SVEALEQGAISWEAPAEKKIECTQKGKSNQTECENFI 114
               :|| | :| :| : :: | | | :| |:|
Qy   131 TLLE-RRSEGLLACGTNARHPSCW--NLVNGTV--VPLGEMRGYAPFSPDENSLVLFEGD 185

Db   115 RFLQPYNSSHLVCGTYAFQPRCTYINMLTFTLDRAEFEDGKGKCPYDPAKGHTGLLVDG 174
               :|| | :| | | : : |: :|| | | :   : | |: :| :|
Qy   186 EVYSTIRKQEYNGKIPRFRRIRGESELIYTSDTV-------MQNPQFIKATIVHQD----QAYDD 238

Db   175 ELYSA-TLNNFLGTEPVILRYMGTHSHSIKTEYLAFWLNEPHVGSARFVPESVGSFTGDDD 233
               :| | |:| | | | | |: : | :: :|| : || : | :| :|
Qy   239 KIYYFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNK 298

Db   234 KIYFFSERAVEYDCYSEQVVARVARVCKGDMGGGARTLQ-KKWTTFLKARLVCSAPDMKV 292
                || | |:| |: || |:| | || || | : ||| || :| | |: :
Qy   299 NFNRLQDVFLLPDPSGQWRDIRVYGVFSNPW---NYSAVCVYSLGDIDKVF------- 346

Db   293 YFNQLKAVHTLRGAS--WHNTTFFGVFQARWGMDMDLSAVCEYQLEQIQQVFEGPYKEYSE 350
                :|| | | | :| :||| | | :| | | | || :: ::| | | | |
Qy   347 RTSSLKGYHSSLPNPRPGKCL--------PDQQPIPTETFQVADRHPEVAQRVEPMGPL 397

Db   351 QAQKWARYTDPVPSPRPGSCINNWHRDNGYTSSLELPDNTLNFIKIHPLMEDQVKPR--L 408
                :| | | :| | | |:| | |: :| ||| | |:||| :| | | : | |
Qy   398 KTPLFHSK-YHYQKVAVHRMQASHGETFHVLYLTTDRGTIIHKVVEPGQEHSFAFNIMEI 456

Db   409 GRPLLVKKNTNFTHVVADRVPGLDGATYTVLFIGTGDGWLLKAVSLGPWIHM---VEEL 464
                | ||::: : :||| | | |: |:|| | |:|:| :|| | ||| :   :|||
Qy   457 QPFRRAAAIQTMSLDAERRKLIVSSQWEVSQVPLDICEVYGGGCHGCLMSRDPYCGW--D 514

Db   465 QVFDQ-EPVESLVLSQSKKVLFAGSRSQLVQLSLADCTKY-RPCVDCVLARDPYCAWNVN 522
                |||| |: :| || ||| | | | | | | | | ||: | |||| ||
Qy   515 QGRCISIYS--SERSVLQSINPAEPHKECP---NPKPDKAPLQKVSLAPNSRYYLSCPMES 570

Db   523 TSRCVATTSGRSGSFLYQHVANLDTSKMCNQYGIKKVRSIPKNITVVSGTDLVLPCHLSS 582
                ||| ::|| |:| | : | :| :| |||: |: | || | :| |:|:|| | ||
Qy   571 RHATYSWRHKENVEQSCEPG---HQSPNCILFIENLTAQQYGHYFCEAQEGSYFREAQHW 627

Db   583 NLAHAHWTFGSQDLPAEOPGSFLYDIGLQALVVMAAQSRHSGPYRC------YSEEQGT 635
                :| | : :|| ||| ||| |: | :| :| | | || |
Qy   628 QLLPEDGIMAEHLLGHACALAAS-------LWLGVLP---TLTLGLLV 665

Db   636 RLAAESYLVAV-VAGSSVTLEARAPLENLGLVWLAVVALGAVCLVLLLV 684
                ||| | |: | |||| | | | ||||:| | | || ||:|::||
Qy   LFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGS----------------------TKGSCLD 122

RESULT 14
T27165

hypothetical protein Y54E5B.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27165
R;Lennard, N.
submitted to the EMBL Data Library, October 1998
R;Reference number: T27165
A;Accession: T27165
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-712 <WIL>
A;Cross-references: EMBL:AL032653; PIDN:CAA21714.1; GSPDB:GN00019; CESP:Y54E5B.1
A;Experimental source: clone Y54E5B
C;Genetics:
C;Gene: CESP:Y54E5B.1
A;Map position: 1
A;Introns: 36/1; 70/2; 85/3; 194/2; 221/1; 253/3; 301/1; 352/3; 522/2; 560/1; 599/3;

Query Match   11.4%; Score 411; DB 2; Length 712;
Best Local Similarity   155; Conservative   80; Mismatches 197; Indels 148; Gaps   30;

Matches   26.7%; Pred. No. 2.7e-23;

Db   36 LLWAAAASAQGHLRSGPRIFAVWKGHVGQDRVD-FGQTEPHTVLFH--EPGSSSVWVGGR 92
                ||| |||:|| :|| | ||| ||| || ||: ||| ||| || | |||||: ||
Qy   30 RLRLLLLLLWAAAASAQG-----HLRSGPRIFAVWKGHVGQDRVDFG-----QTEPHTV 77

Db   93 GKVY-----LFDFPEGKNASVRTVNIGSTKGSCL---DKRDCENYITLLER-RSEGLLACG 144
                ||| |||||||||||||| ||:||||| | |:||||| | || : || | |
Qy   78 LFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGS-------------------TKGSCLD 122

Db   145 TNARHPSC--WNLVNGTVVPLGEM--RGYAPFSPDENSLVLFEGDEVYSTIRKQEYNGKI 200

Db   127 TNAYKPLCRHYALRDGDYVVEKEYEGRGLCPFDPDHNSTAIYSEGQLYSA-TVADFSGTD 185

Qy   201 PRFRRIRGESELYTSDTVMQN-PQFIKATIVHQDQAYDKIYYFREDNPDKNPEAPLNV 259

Db   186 PLI--YRGPLRTERSDLKQLNAPNPNVNT----MEYNDFIFFFRETAVEYINCGKAIY 237

Qy   260 SRVAQLCRGDQGGESSLSVSKWNTFLKAMLVCSDAATNK-NFNRLQDVF-LLPDPSGQWR 317

Db   238 SRVARVCKHDKGGPHQFG-DRWTSFLKSRLNCSVPGDYPFYFNEIQSTSDIIEGNYGGQV 296

Qy   318 DIRVYGVFSNPWNY---SAVCVYSLGDIDKVF----------------------RTSSLKGYHSSLP 359

Db   297 EKLIYGVFTTPVNSIGGSAVCAFSMKSILESFDGPFKEQETMNSNWLAVPSLK----VP 351

Qy   360 NPRGKCLFDQQIPTETFQVADRHPEVAQRVEPMGPLKTPLFHSK-------YHYQK 410

Db   352 EPRPGQCVNDSRTLPDVSVNFVKSHTLMDEAV------------PAFFTRPILIRISLQYRFTK 403

Qy   411 VAV-HRMQASHGETFHVLYLTTDRGTIIHKVVEPGQEHSFAFN---IMEIQPFRRAAAIQ 466

Db   404 IAVDQQVRTPDGKAVDVLFIGTDDGKVIRALNSASFDSDSDTVDSVVIEELQVLPPGVPVK 463

Qy   467 TM---SLDAERRKLIVSSQWEVSQVPLDLCEVYGG-----GCHGCLMSRDPYCGWD---QGR 517

Db   464 NLYVVRMDGDDSKLVVVSDDEILATKLHRC---GSDKITNCRECVSLQDDYCAWDNVELK 520

Qy   518 CISIYS------SERSVLQSINPAEPHKEC 541

Db   521 CTAVGSPDWSAGKRRFIQNISLGE-HKAC 548

Qy   78 LFHEPGSSSVWVGGRGKVYLFDFPEGKNASVRTVNIGS----------------------TKGSCLD 122

RESULT 15
JC5928

semaphorin F precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000
C;Accession: JC5928
R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.
Biochem. Biophys. Res. Commun. 242, 685-691, 1998
A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candi
A;Reference number: JC5928; MUID:98125554; PMID:9464278
A;Accession: JC5928
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1074 <SIM>
A;Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584
A;Experimental source: brain
A;Comment: This protein disrupts normal brain development and leads to some of the featu

A;Superfamily: semaf
A;Gene: semaf
A;Genetics:
C;Superfamily:
F;971-993/Domain: transmembrane #status predicted <TMM>
F;840-896/Domain: thrombospondin type 1 repeat homology <THR>
F;50-533/Domain: semaphorin #status predicted <SEM>
F;1-20/Domain: signal sequence #status predicted <SIG>
C;Superfamily: human semaphorin F; thrombospondin type 1 repeat homology

Query Match 11.3%; Score 409; DB 2; Length 1074;
Best Local Similarity 29.5%; Pred. No. 7e-23;
Matches 147; Conservative 76; Mismatches 206; Indels 70; Gaps 28;

```
Qy   64 QDRVDFGQOTEPHTVLFHEPGSSSVWWGRGRKVYLFDFPEGKNASVRTVN--IGSTKGSC 120
Db   53 KNAADFSQ------LTFDPGGKELVVGARN-YLFRLQLEDLSLIQAVEWECDEATKKAC 104

Qy  121 L----DKRDCENYITLLERRSEGLLACGTNARHPSCWNLVNGTVVPL-GEMRGYA-PFS 173
Db  105 YSKGKSKEECQNYIRVLLVGGDRLFTCGTNAFTPVCTNRSLSNLAEIHDQISGMARCPYS 164

Db   57 LLAADG-DSLLVGARNAV------NLSLSTLSVNHKIDWKPPAEHIEECIMKGK--S 105

Qy  123 KRDCENYITLLERRSEGL-LACGTNARHPSCWNLVNGTVVPLG------EMRGYAPFSP 174
Db  106 KTDCQNYIRVLARKSAGVSLVCGTHAFSPKCREY---TVTEFGIRNTRQFDGQGISPYDP 162

Qy  175 DENSLVL-------------FEGDE--VY------STIRKQEYNGKIPRFR 204
Db  163 KHNSSALYVPGTNQLFVATVTDFVGNDALIYRKTIDETPSSKSAANIRTQSYDAR---- 217

Qy  205 RIRGESELYTSDTVWQNPQFIKATIVHQDQAYDDKIYYFRE--DNPDKNPEAPLNVSRV 262
Db  218 ------------VLNAPNFV-ATF-----AYKEHVYFWFREIASEAIDNNEEPQIYARV 258

Qy  263 AQLCRGDQGGESSLSVSKWNTFLKAMLVCS--DAATNKNFNRLQDVFLLPDDPSGQWRDTR 320
Db  259 ARVCKNDKGGARPAN-ERWTSYLKARLNCSLPSGSSPFYNELKAV---SDPIDAGNNNH 314

Qy  321 -VYGVFSNP---WNYSAVCVYSLSGDIIDKVFRTSSLKGYHSS-----------LPNRPGK 365
Db  315 VVYTVFSTPDSDVRMSAVCKFSMKKITREEFDNGTFKHQNNAQSMWWAFNRNEVPKPRPGS 374

Qy  366 CLPDQOPIPTETFQVVADRHPEVAQRVEPMGPLKTPLFHSKYH---YQKVAVHRMQAASHG 421
Db  375 CSPDSTKLPENTVSFLHPLLHR---PIPSVAAPLLVEGADRADLTQITVLPVRAVGG 431

Qy  422 ETFHVLYLTTDRGTIHKVVEPEGEQEHSFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSS 481
Db  432 HNYDILFIGTSDGKVLKVVEVDGN---ATVIQSATVFQRGVPI--VNLLTKESVVIVS 485

Qy  482 QWEVSQVPLDLCEVYGGGCHGCLMSRDPYCGWDQ--GRCI 519
Db  486 ADEIASLPVHNC-AQQTSCSKCVQLQDPHCAWDSSIARCV 524

Qy  174 PDENSLVLF-EGDEVYSTIRKQEYNGKIPRFRRIRG-----ESELYTSDTIVMQNPQFIKA 227
Db  165 PQHNSTALLITAGGELYAA-TAMDFPGRDPAIYRSLGILPPLRTAQYNSKW-LNEPNFV-- 220

Qy  228 TIVHQDQAYD--DKIYYFFREDNPDKNPEAPLNVSRVAQLCRGDQGGESSLSVSKWNTFPL 285
Db  221 ---SSYDIGNFTYFFRE-NAVEHDCGKTVFSRAARVCKNDIGGRFLLE-DTWTTFM 272

Qy  286 KAMLVCS-DAATNKNFNRLQDVFLLPDDPSGQWRDTRVGVFSNPWN---YSAVCVYSLGD 341
Db  273 KARLNCSRRGEVPFYYNELQSTFFLPELD-----LIYGIFTTNVVNSIAASAVCVFNLSA 326

Qy  342 IDKVFRTSSLKGYHSS-------LPNPRPG-KCLPDQOPIPTETFQVVADRHPEVAQRV--- 391
Db  327 IAQAF-SGPFKYQENSRSSAWLPYPNPNHFQCGTVDQGL---YVNLTERNLQDDAQKFILV 382

Qy  392 -EPMGPLKT-PLF-HSKYHYQKVAVHRMQAASHGETFHVLYLTTDRGTIHKVVEP-GEQEH 447
Db  383 HEVVQPVTIVPSFMEDNSRFSHVAVDVVQGREA-LVHIIYLATDYGTIKKVRVPLNQYSS 441

Qy  448 SFAFNIMEIQPFRRAAAIQTMSLDAERRKLYVSSQWEVSQVPLDLCEVYGGGCCHGCLMSR 507
Db  442 SCLLEEIELFPERRREPIRSLQIIHSQSVLFVGLREHVKIPLKRCQFYRTR-STCIGAQ 500

Qy  508 DPYCGWD--QGRCISIYSS 524
Db  501 DPYCGWDVVMKKCTSLEES 519
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Search completed: March 14, 2003, 09:27:40
Job time : 24.4774 secs